

RESULT 1
IL2B_PIG
ID IL2B_PIG STANDARD; PRT; 324 AA.
AC Q28938;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE maturation factor 40 kDa subunit) (CLMF p40).
GN IL2B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97383978; PubMed=9239844;
RA Foss D.L., Murtaugh M.P.;
RT "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL Vet. Immunol. Immunopathol. 57:121-134(1997).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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DR EMBL; U08317; AAA75356.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 324 INTERLEUKIN-12 BETA CHAIN.
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 231 316 FIBRONECTIN TYPE-III.
FT DISULFID 50 90 POTENTIAL.
FT DISULFID 195 195 INTERCHAIN (PROBABLE).
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 324 AA; 36828 MW; F0E48B72F700086C CRC64;

Query Match 90.7%; Score 1578; DB 1; Length 324;
Best Local Similarity 90.7%; Pred. No. 1.8e-127;
Matches 291; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 4 QQLVISWFSVLVLLASPLMAIWELKKDVIYVVELDWYPNAPGETVVLTCDTPEEDGITWTS 63
Db 4 QQLVVSWSFSLVWLASPIVAIWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITWTS 63

QY 64 QSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGEALSRSLLLKKKEDGIWSTDILKDOKEP 123
Db 64 QSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVLSQSLLLLKKKEDGIWSTDILKDOKEP 123

QY 124 KNKSFLKCEAKNYSGRFTCWLLTISTDLKFSVKSSRGSTDPRGVTCTATLSEDLGEYK 183
Db 124 KNKSFLKCEAKNYSGRFTCWLLTAISTDLKFSVKSSRGSTDPRGVTCTATLSEDLGEYK 183

QY 184 KYRVECEQGSACPAAEESLPIEVVLEAVHKLKYENYTSSFFIRDIKPDPPKNLQKLPLK 243
Db 184 KYRVECEQGSACPAAEESLPIEVVLEAVHKLKYENYTSSFFIRDIKPDPPKNLQKLPLK 243

QY 244 NSRHVEVSWGYPTWTWSTPHSYFSLTFQIQVGKSKREKKDRIFTDKTSATVICRKNKAKIR 303
Db 244 NSRHVEISWEYPTWTWSTPHSYFSLMFGVQVGKSKREKKDKLFTDQISAKVTCHKDANIR 303

QY 304 VQARDRIYSSFWSEWASVSCS 324
Db 304 VQARDRIYSSSWSEWASVSCN 324

RESULT 14
 AR052857
 LOCUS AR052857 1018 bp DNA linear PAT 29-SEP-1991
 DEFINITION Sequence 194 from patent US 5833975.
 ACCESSION AR052857
 VERSION AR052857.1 GI:5977719
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 1018)
 AUTHORS Paoletti, E., Tartaglia, J. and Cox, W.I.
 TITLE Canarypox virus expressing cytokine and/or tumor-associated antigen
 JOURNAL DNA sequence
 Patent: US 5833975-A 194 10-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..1018
 /organism="unknown"
 BASE COUNT 283 a 245 c 260 g 230 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.77e-142 Length: 1018
 Score: 1539.00 Matches: 288
 Percent Similarity: 92.10% Conservative: 15
 Best Local Similarity: 87.54% Mismatches: 20
 Query Match: 88.45% Indels: 6
 DB: 6 Gaps: 2

US-09-725-324A-8 (1-324) x AR052857 (1-1018)

Qy 1 MetCysHisGlnGlnLeuValIleSerTrpPheSerLeuValLeuLeuAlaSerProLeu 20
 Db 32 ATGTGTCAACAGCAGTGTGGTCATCTCTGGTTTCCCTGGTCTTCTGGCATCTCCCTC 91
 Qy 21 MetAlaIleTrpGluLeuLysLysAspValTyrValValGluLeuAspTrpTyrProAsn 40
 Db 92 GTGGCCATATGGGAAGTGAAGAAAGATGTTATGTCGTAGAAATTGGATGGTATCCGGAT 151
 Qy 41 AlaProGlyGluThrValValLeuThrCysAspThrProGluGluAspGlyIleThrTrp 60
 Db 152 GCCCTGGAGAAATGGTGGTCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211
 Qy 61 ThrSerAspGlnSerSerGluValLeuGlyThrGlyLysThrLeuThrIleHisValLys 80
 Db 212 ACCTTGGACCAAGAGCAGTGGAGTCTTAGGCTCTGGCAAAACCTGACCATCAAGTCAAA 271
 Qy 81 GluPheGlyAspAlaGlyGlnTyrThrCysArgLysGlyGlyGluAlaLeuSerArgSer 100
 Db 272 GAGTTTGGAGATGCTGGCCAGTACACCTGTACAAAGGAGGCGAGGTCTAAGCCATTGC 331
 Qy 101 LeuLeuLeuLeuHisLysLysGluAspGlyIleTrpSerThrAspIleLeuLysAspGln 120
 Db 332 CTCCTGCTGCTTCACAAAAGGAAGATGGAATTTGGTCCACTGATATTTAAAGGACCAG 391
 Qy 121 LysGluProLysAsnLysSerPheLeuLysCysGluAlaLysAsnTyrSerGlyArgPhe 140
 Db 392 AAAGAACCACAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATCTGGACGTTTC 451
 Qy 141 ThrCysTrpTrpLeuThrThrIleSerThrAspLeuLysPheSerValLysSerSerArg 160
 Db 452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTGACATTGACGTGCAAAAGCAGCAGA 511
 Qy 161 GlySerThrAspProArgGlyValThrCysGlyThrAlaThrLeuSerGlu----- 177
 Db 512 GGCTCTTCTGACCCCAAGGGGTGACGTGCGGAGCTGTACACTCTCTGCAGAGAGAGTC 571
 Qy 178 -----AspLeuGlyGluTyrLysLysTyrArgValGluCysGlnGluGlySerAlaCys 195
 Db 572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628
 Qy 196 ProAlaAlaGluGluSerLeuProIleGluValValLeuGluAlaValHisLysLeuLys 215
 Db 629 CCAGCTGCTGAGGAGAGTCTGCCATTGAGGTTCATGGTGGATGCCGTTCAAGCTCAAG 688
 Qy 216 TyrGluAsnTyrThrSerSerPhePheIleArgAspIleIleLysProAspProProLys 235
 Db 689 TATGAAACTACACAGCAGCTTCTTCATCAGGGACATCATCAACCTGACCCACCCCAAG 748
 Qy 236 AsnLeuGlnLeuLysProLeuLysAsnSerArgHisValGluValSerTrpGlyTyrPro-255
 Db 749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTGAGTGGAGTACCCT 808
 Qy 256 AspThrTrpSerThrProHisSerTyrPheSerLeuThrPheCysIleGlnValGlnGly 275
 Db 809 GACACCTGGAGTACTCCACATTCTACTCTCCCTGACATTCTGCGTTGAGGTCCAGGGC 868
 Qy 276 LysSerLysArgGluLysLysAspArgIlePheThrAspLysThrSerAlaThrValIle 295
 Db 869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928
 Qy 296 CysArgLysAsnAlaLysIleArgValGlnAlaArgAspArgTyrTyrSerSerPheTrp 315
 Db 929 TGCCGCAAAATGCCAGCATTAGCGTGGGGCCAGGACCGCTACTATAGTCTATCTTGG 988
 Qy 316 SerGluTrpAlaSerValSerCysSer 324
 Db 989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015